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ATTORNEY DOCKET NO. 21101.0021P1

SEQUENCE LISTING

<110> University of Utah Research Foundation
Bock, Susan C.
Hobden, Adrian N.

<120> VARIANTS OF ANTITHROMBIN III

<130> 21101.0021P1

<150> 60/384,599

<151> 2002-05-31

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<211> 54
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<210> 57

<211> 54

<212> DNA

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<210> 58

<211> 54

<212> DNA

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<210> 61

<211> 54

<212> DNA

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<210> 62

<211> 54

<212> DNA

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<210> 63

<211> 54

<212> DNA

<213> Artificial Sequence

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<400> 63

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<210> 64

<211> 54

<212> DNA

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<212> DNA

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<210> 66
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<210> 67
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<210> 69
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 Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
 20 25 30
 Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
 35 40 45
 Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
 50 55 60
 Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser Pro Leu Ser
 65 70 75 80
 Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
 85 90 95
 Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
 100 105 110
 Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
 115 120 125
 Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
 130 135 140
 Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
 145 150 155 160
 Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
 165 170 175
 Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
 180 185 190
 Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
 195 200 205
 Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
 210 215 220
 Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
 225 230 235 240
 Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
 245 250 255
 Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
 260 265 270
 Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
 275 280 285
 Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
 290 295 300
 Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
 305 310 315 320
 Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
 325 330 335
 Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
 340 345 350
 Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
 355 360 365
 Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
 370 375 380
 Ala Leu Glu Ala Asn Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
 385 390 395 400
 Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
 405 410 415
 Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 71

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<211> 29
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<400> 71
cagagatctc acgggagcct gtggacatc 29

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<400> 73
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ctgtctagat tacttaaacac aagggttggc tac 33

<210> 75
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ctatcgaaaa gccaacaaag cctccaagg tt agtatcagc 39

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Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20 25 30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35 40 45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50 55 60
Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser Pro Leu Ser
65 70 75 80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85 90 95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100 105 110
Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
115 120 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130 135 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145 150 155 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165 170 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
180 185 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
195 200 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
210 215 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225 230 235 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
245 250 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
260 265 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
275 280 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
290 295 300
Trp Leu Asp Glu Leu Glu Met Met Leu Val Val His Met Pro Arg
305 310 315 320

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Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
 325 330 335
 Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
 340 345 350
 Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
 355 360 365
 Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
 370 375 380
 Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
 385 390 395 400
 Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
 405 410 415
 Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 78

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 78

Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
 1 5 10 15
 Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
 20 25 30
 Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
 35 40 45
 Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
 50 55 60
 Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser Pro Leu Ser
 65 70 75 80
 Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
 85 90 95
 Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
 100 105 110
 Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
 115 120 125
 Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
 130 135 140
 Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
 145 150 155 160
 Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
 165 170 175
 Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
 180 185 190
 Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
 195 200 205
 Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
 210 215 220
 Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
 225 230 235 240
 Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
 245 250 255
 Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
 260 265 270
 Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
 275 280 285

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Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
 290 295 300
 Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
 305 310 315 320
 Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
 325 330 335
 Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
 340 345 350
 Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
 355 360 365
 Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
 370 375 380
 Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
 385 390 395 400
 Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
 405 410 415
 Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 79

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 79

agccctgtgg acatctgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt	60
taccgctccc cggagaagaa ggcaactgag gatgagggtc cagaacagaa gatccccggag	120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgcgttgc taccactttc	180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt	240
atctccacgg cttttgtctat gaccaagctg ggtgcctgtc atgacacccct ccagcaactg	300
atggaggtat ttaagttga caccatatct gagaaaaacat ctgatcagat ccacttcttc	360
tttgccaaac tgaactgccc actctatcga aaagccaaca aagcctccaa gtagtatca	420
gccaatcgcc tttttggaga caaatccctt accttcaatg agaccttca ggacatcagt	480
gagttggtat atggagccaa gctccagccc ctggacttca agggaaatgc agagcaatcc	540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt	600
cctctggaaag ccatcaatga gtcactgtt ctggtgctgg ttaacaccat ttacttcaag	660
ggcctgtgga agtcaaaggat cagccctgag aacacaagga aggaactgtt ctacaaggct	720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagtccg ttatcggcgc	780
gtggctgaag gcacccagggt gtttggatgg cccttcaaag gtgatgacat caccatggtc	840
ctcatcttgc ccaaggctga gaagagccgtg gccaagggtgg agaaggaact caccctcagag	900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc	960
ttccgcattt aggacggctt cagtttgaag gagcagctgc aagacatggg ctttgtcgat	1020
ctgttcagcc ctgaaaaggat caaactccca ggtattgtt cagaaggccg agatgacctc	1080
tatgtctcaag atgcatttcca taaggcattt cttggaggtaa atgaagaagg cagtgaagcg	1140
gccgcaagta ccgcctctaga ggctcaggcc cgatcgctaa accccaaacag ggtgactttc	1200
aaggccaaaca ggccttccct gttttttata agagaagtcc ctctgaacac tattatcttc	1260
atgggcagag tagccaaaccc ttgtgttaag taa	1293

<210> 80

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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<400> 80

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agtcccgtag atatatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt      60
taccgctccc cgagaagaa gcaactgag gatgagggtc cagaacagaa gatcccggag     120
gccaccaacc ggcgtgtctg gaaactgtcc aaggccaatt cccgcttgc taccactttc     180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt    240
atctccacgg cttttctat gaccaagctg ggtgcctgtc atgacaccct ccagcaactg    300
atggaggtat ttaagttga caccatattc gagaaaacat ctgatcagat ccacttcttc    360
tttgccaaac tgaactgccc actctatcga aaagccaaca aagcctccaa gtttagtatca   420
gccaatcgcc ttttggaga caaatccctt accttcaatg agacctacca ggacatcagt   480
gagttggat atggagccaa gtcaggccc ctggacttca aggaaaatgc agagcaatcc   540
agagcggcca tcaacaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt  600
ccctcggaaag ccatcaatga gtcactgtt ctggtgcgtt ttaacaccat ttacttcaag  660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct  720
gatggagagt cgtgtcagc atctatgat taccaggaag gcaagtccg ttatcggcgc  780
gtggctgaag gcaccagggt gctttagttt cccttcaaaag gtgatgacat caccatggtc 840
ctcatcttgc ccaaggctga gaagagctg gccaagggtgg agaaggaact caccaggag 900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tgggtgttca catgccccgc 960
ttccgcattt aggacggctt cagtttgaag gagcagctgc aagacatggg cttgtcgat 1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgtt cagaaggccg agatgacctc 1080
tatgtctcaag atgcatttca taaggcattt cttaggtt aaatgaaagg cagtgaagcg 1140
gccgcaagta cgcctctaga ggctcaggc cggtcgctaa accccaacag ggtgactttc 1200
aaggccaaca ggccttcctt ggttttata agagaagttc ctctgaacac tattatcttc 1260
atggcagag tagccaaaccc ttgtgttaag taa 1293

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<210> 81

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 81

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Ser Pro Val Asp Val Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1           5          10          15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20          25          30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35          40          45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50          55          60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65          70          75          80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85          90          95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100         105         110
Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
115         120         125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130         135         140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145         150         155         160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165         170         175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
180         185         190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
195         200         205

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Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
 210 215 220
 Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
 225 230 235 240
 Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
 245 250 255
 Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
 260 265 270
 Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
 275 280 285
 Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
 290 295 300
 Trp Leu Asp Glu Leu Glu Met Met Leu Val Val His Met Pro Arg
 305 310 315 320
 Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
 325 330 335
 Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
 340 345 350
 Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
 355 360 365
 Ala Phe Leu Glu Val Asn Glu Gly Ser Glu Ala Ala Ala Ser Thr
 370 375 380
 Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
 385 390 395 400
 Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
 405 410 415
 Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 82

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 82
 agccctgtgg acgtatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt 60
 taccgcgtccc cggagaagaa ggcaactgag gatgagggtct cagaacagaa gatcccgag 120
 gccacccaacc ggcgtgtctg ggaactgtcc aaggccatt cccgcttgc taccactttc 180
 tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt 240
 atctccacgg cttttcttat gaccaagctg ggtgcctgtt atgacaccct ccagcaactg 300
 atggaggtat ttaagtttg a cccatatct gagaaaaacat ctgatcagat ccacttcttc 360
 ttgcacaaac tgaactgccc actctatcga aaagccaaaca aagcctccaa gttatgtatca 420
 gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt 480
 gagtttgtat atggagccaa gctccagccc ctgacttca aggaaaatgc agagcaatcc 540
 agagcggcca tcaacaaatg ggtgtccaaat aagaccgaag gccgaatcac cgatgtcatt 600
 ccctcgaaag ccatcaatga gtcactgtt ctgtgtctgg ttaacaccat ttacttcaag 660
 ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct 720
 gatggagagt cgtgttcagc atctatgtt taccaggaaag gcaagtccg ttatcgccgc 780
 gtggctgaag gcacccaggt gcttgagggt cccttcaaag gtatgacat caccatggtc 840
 ctcatcttgc ccaagcctga gaagagctg gccaagggtgg agaaggaact caccggcag 900
 gtgcgtcagg agtggctgga tgaattggag gagatgtgc tgggtgtcca catgccccgc 960
 ttccgcattt aggacggctt cagtttgaaag gagcagctgc aagacatggg ccttgcgt 1020
 ctgttcagcc ctgaaaagtc caaactccca ggtattgtt cagaaggccg agatgacctc 1080
 tatgtctcag atgcatttca taaggcattt ctggaggtaa atgaagaagg cagtgaagcg 1140
 gcccgaagta cccgtctaga ggctcaggcc cggtcgctaa accccaacag ggtgactttc 1200
 aaggccaaca ggccttcctt ggttttata agagaagttc ctctgaacac tattatcttc 1260
 atgggcagag tagccaaaccc ttgtgttaag taa 1293

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<210> 83
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 83

agtcccgtag	atgtgtcac	agccaagccg	cgggacattc	ccatgaatcc	catgtgcatt	60
taccgtctcc	cgagaagaa	ggcaactgag	gatgagggt	cagaacagaa	gatcccgag	120
gccaccaacc	ggcgtgtctg	gaaactgtcc	aaggccaatt	cccgcttgc	taccactttc	180
tatcagcacc	tggcagattc	caagaatgac	aatgataaca	ttttcctgtc	acccttgagt	240
atctccacgg	cttttgcata	gaccaagctg	ggtgcctgt	atgacaccct	ccagcaactg	300
atggaggtat	ttaagttga	caccatatct	gagaaaaacat	ctgatcagat	ccacttcttc	360
tttgc当地	tgaactgccc	actctatcga	aaagccaaca	aagcctccaa	gttagtatca	420
gccaatcgcc	tttttggaga	caaatccctt	accctcaatg	agacctacca	ggacatcagt	480
gagtttgtat	atggagccaa	getccagccc	ctgacttca	aggaaaatgc	agagcaatcc	540
agagcggcca	tcaacaaatg	ggtgtccaaat	aagaccgaag	gccgaatcac	cgtgtcatt	600
ccctcgaaag	ccatcaatga	gtcactgtt	ctggcgtctgg	ttaacaccat	ttacttcaag	660
ggcctgtgga	agtcaaagt	cagccctgag	aacacaagga	aggaactgtt	ctacaaggct	720
gatggagagt	cgtgttcage	atctatgat	taccaggaag	gcaagtccg	ttatcgccgc	780
gtggctgaag	gcacccaggt	gctttaggtt	cccttcaaag	gtgatgacat	caccatggtc	840
ctcatcttgc	ccaaggctga	gaagagcctg	gccaagggtgg	agaaggaact	caccccgag	900
gtgctgcagg	agtggctgga	tgaattggag	gagatgatgc	tggtggtcca	catgccccgc	960
ttccgcattt	aggacggctt	cagtttgaag	gaggcagctgc	aagacatggg	ccttgcgtat	1020
ctgttcagcc	ctgaaaagtc	caaactccca	ggtattgtt	cagaaggccg	agatgacctc	1080
tatgtctcag	atgcattcca	taaggcattt	cttgaggtaa	atgaagaagg	cagtgaagcg	1140
gccgcaagta	ccgctctaga	ggctcaggc	cgttcgctaa	accccaacag	ggtgacttcc	1200
aaggccaaaca	ggcctttcct	ggtttttata	agagaagtcc	ctctgaacac	tattatcttc	1260
atggcagag	tagccaaaccc	tttgtgttaag	taa			1293

<210> 84
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 84

Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
1				5				10				15			
Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu		
				20				25				30			
Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp	Glu
				35				40				45			
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His	Leu
				50				55				60			
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Ile	Phe	Leu	Ser	Pro	Leu	Ser	
	65				70				75				80		
Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp	Thr
				85				90				95			
Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu	Lys
				100				105				110			
Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu	
				115				120				125			

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Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
 130 135 140
 Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
 145 150 155 160
 Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
 165 170 175
 Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
 180 185 190
 Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
 195 200 205
 Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
 210 215 220
 Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
 225 230 235 240
 Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
 245 250 255
 Arg Tyr Arg Arg Val Ala Glu Gly Thr Gin Val Leu Glu Leu Pro Phe
 260 265 270
 Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
 275 280 285
 Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
 290 295 300
 Trp Leu Asp Glu Leu Glu Met Met Leu Val Val His Met Pro Arg
 305 310 315 320
 Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
 325 330 335
 Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
 340 345 350
 Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
 355 360 365
 Ala Phe Leu Glu Val Asn Glu Gly Ser Glu Ala Ala Ala Ser Thr
 370 375 380
 Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
 385 390 395 400
 Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
 405 410 415
 Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 85

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 85

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1 5 10 15
 Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
 20 25 30
 Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
 35 40 45
 Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
 50 55 60
 His Leu Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser Pro
 65 70 75 80
 Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
 85 90 95

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Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
 100 105 110
 Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
 115 120 125
 Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
 130 135 140
 Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
 145 150 155 160
 Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
 165 170 175
 Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
 180 185 190
 Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
 195 200 205
 Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
 210 215 220
 Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
 225 230 235 240
 Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
 245 250 255
 Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
 260 265 270
 Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
 275 280 285
 Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
 290 295 300
 Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
 305 310 315 320
 Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
 325 330 335
 Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
 340 345 350
 Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
 355 360 365
 His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
 370 375 380
 Ser Thr Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val
 385 390 395 400
 Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
 405 410 415
 Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 86

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 86

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1 5 10 15
 Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
 20 25 30
 Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
 35 40 45

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Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
 50 55 60
 His Leu Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser Pro
 65 70 75 80
 Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
 85 90 95
 Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
 100 105 110
 Glu Lys Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys
 115 120 125
 Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
 130 135 140
 Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
 145 150 155 160
 Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
 165 170 175
 Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
 180 185 190
 Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
 195 200 205
 Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
 210 215 220
 Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
 225 230 235 240
 Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
 245 250 255
 Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
 260 265 270
 Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
 275 280 285
 Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
 290 295 300
 Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
 305 310 315 320
 Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
 325 330 335
 Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
 340 345 350
 Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
 355 360 365
 His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
 370 375 380
 Ser Thr Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val
 385 390 395 400
 Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
 405 410 415
 Leu Asn Thr Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 87

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 87

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1 5 10 15

ATTORNEY DOCKET NO. 21101.0021P1

Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
 20 25 30
 Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
 35 40 45
 Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
 50 55 60
 His Leu Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser Pro
 65 70 75 80
 Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
 85 90 95
 Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
 100 105 110
 Glu Lys Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys
 115 120 125
 Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
 130 135 140
 Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
 145 150 155 160
 Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
 165 170 175
 Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
 180 185 190
 Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
 195 200 205
 Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
 210 215 220
 Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
 225 230 235 240
 Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
 245 250 255
 Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
 260 265 270
 Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
 275 280 285
 Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
 290 295 300
 Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
 305 310 315 320
 Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
 325 330 335
 Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
 340 345 350
 Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
 355 360 365
 His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
 370 375 380
 Ser Thr Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val
 385 390 395 400
 Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
 405 410 415
 Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 88

<211> 423

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =

ATTORNEY DOCKET NO. 21101.0021P1

synthetic construct

<400> 88

Arg	Asp	Ile	Pro	Val	Asn	Pro	Ile	Cys	Ile	Tyr	Arg	Asn	Pro	Glu	Lys	
1							5		10					15		
Lys	Pro	Gln	Glu	Arg	Arg	Gly	Ala	Gly	Ala	Gly	Glu	Gly	Gln	Asp	Pro	
							20		25					30		
Gly	Val	His	Lys	Pro	Pro	Val	Trp	Glu	Leu	Ser	Arg	Ala	Asn	Ser	Arg	
							35		40					45		
Phe	Ala	Val	Val	Phe	Tyr	Lys	His	Leu	Ala	Asp	Ser	Lys	Asp	Asn	Glu	
							50		55					60		
Glu	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser	Ile	Ser	Thr	Ala	Phe	Ala	Met	
							65		70					80		
Thr	Lys	Leu	Gly	Ala	Cys	Gly	Asp	Thr	Leu	Gln	Gln	Leu	Met	Glu	Val	
							85		90					95		
Phe	Gln	Phe	Asp	Thr	Ile	Ser	Glu	Lys	Thr	Ser	Asp	Gln	Val	His	Phe	
							100		105					110		
Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu	Tyr	Lys	Lys	Ala	Asn	Lys	Ser	
							115		120					125		
Ser	Glu	Leu	Ile	Ser	Ala	Asn	Arg	Leu	Phe	Gly	Glu	Lys	Ser	Leu	Val	
							130		135					140		
Phe	Asn	Glu	Thr	Tyr	Gln	Ile	Ser	Glu	Ile	Val	Tyr	Gly	Ala	Lys		
							145		150					160		
Leu	Trp	Pro	Leu	Asn	Phe	Lys	Glu	Lys	Pro	Glu	Leu	Ser	Arg	Lys	Ile	
							165		170					175		
Ile	Asn	Glu	Trp	Val	Ala	Asn	Lys	Thr	Glu	Arg	Arg	Ile	Thr	Glu	Val	
							180		185					190		
Ile	Pro	Glu	Lys	Gly	Ile	Asp	Asp	Leu	Thr	Val	Leu	Val	Leu	Val	Asn	
							195		200					205		
Thr	Ile	Tyr	Phe	Lys	Gly	His	Trp	Lys	Ser	Gln	Phe	Pro	Ala	Pro	Asn	
							210		215					220		
Thr	Arg	Leu	Asp	Leu	Phe	His	Lys	Ala	Asn	Gly	Glu	Thr	Cys	Asn	Val	
							225		230					235		240
Pro	Ile	Met	Tyr	Gln	Glu	Ser	Arg	Phe	Pro	Tyr	Ala	Phe	Ile	Gln	Glu	
							245		250					255		
Asp	Lys	Val	Gln	Val	Leu	Glu	Leu	Pro	Tyr	Lys	Gly	Asp	Asp	Ile	Thr	
							260		265					270		
Met	Val	Leu	Val	Leu	Pro	Lys	Ala	Gly	Thr	Pro	Leu	Val	Glu	Val	Glu	
							275		280					285		
Arg	Asp	Leu	Thr	Ser	Asp	Lys	Leu	Gln	Asp	Trp	Ile	Asp	Ser	Met	Met	
							290		295					300		
Glu	Val	Ser	Leu	Thr	Val	Ser	Phe	Pro	Arg	Phe	Arg	Val	Glu	Asp	Ser	
							305		310					315		320
Phe	Ser	Val	Lys	Glu	Lys	Leu	Arg	Lys	Met	Gly	Leu	Glu	Asp	Leu	Phe	
							325		330					335		
Ser	Pro	Glu	Asn	Ala	Lys	Leu	Pro	Gly	Ile	Val	Ala	Gly	Asp	Arg	Thr	
							340		345					350		
Asp	Leu	Tyr	Val	Ser	Glu	Ala	Phe	His	Lys	Ala	Phe	Leu	Glu	Val	Asn	
							355		360					365		
Glu	Glu	Gly	Ser	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Val	Ile	Ser	Gly	
							370		375					380		
Arg	Ser	Phe	Pro	Met	Asn	Arg	Ile	Ile	Phe	Glu	Ala	Asn	Arg	Pro	Phe	
							385		390					395		400
Leu	Leu	Phe	Ile	Arg	Glu	Ala	Thr	Leu	Asn	Thr	Ile	Ile	Phe	Met	Gly	
							405		410					415		
Arg	Ile	Ser	Asp	Pro	Cys	Ser										
							420									

<210> 89

<211> 456

ATTORNEY DOCKET NO. 21101.0021P1

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 89
 Met Tyr Leu Leu Ser Leu Leu Leu Ser Leu Leu Gly Ser Ala Tyr
 1 5 10 15
 Leu Gln Pro Gln His Ala Asp Ile Cys Leu Ala Lys Pro Lys Asp Ile
 20 25 30
 Pro Leu Thr Pro Met Cys Val Tyr Arg Lys Pro Leu Glu Val Val Glu
 35 40 45
 Thr Glu Glu Lys Glu Lys Glu Pro Thr Thr Gln Glu Gln Lys Val Pro
 50 55 60
 Glu Ser Thr Asn Pro Arg Val Tyr Glu Leu Ser Gln Ala Asn Ala Lys
 65 70 75 80
 Phe Ala Ile Ala Phe Tyr Lys Asn Leu Ala Asp Ser Lys Arg Asp Lys
 85 90 95
 Glu Asn Ile Phe Met Ser Pro Leu Ser Ile Ser Gln Ala Phe Thr Met
 100 105 110
 Ala Lys Leu Gly Ala Cys Asn Asn Thr Leu Lys Gln Leu Met Glu Val
 115 120 125
 Phe His Phe Asp Thr Val Ser Glu Arg Ala Ser Asp Gln Ile His Tyr
 130 135 140
 Phe Phe Ala Lys Leu Asn Cys Arg Leu Phe Arg Lys Ala Asn Lys Ser
 145 150 155 160
 Ser Glu Leu Val Ser Val Asn Arg Leu Phe Gly Glu Lys Ser Leu Thr
 165 170 175
 Phe Asn Glu Thr Tyr Gln Asp Ile Ser Glu Ile Val Tyr Gly Ala Lys
 180 185 190
 Leu Trp Pro Leu Asn Phe Arg Asp Lys Pro Glu Leu Ser Arg Glu Ile
 195 200 205
 Ile Asn Asn Trp Val Ser Asn Lys Thr Glu Lys Arg Ile Thr Asp Val
 210 215 220
 Ile Pro Lys Asp Ala Ile Thr Pro Asp Thr Val Leu Val Leu Ile Asn
 225 230 235 240
 Ala Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Asn Ser Glu Asn
 245 250 255
 Thr Lys Met Asp Gln Phe His Pro Ala Lys Asn Ser Asn Cys Leu Thr
 260 265 270
 Ala Thr Met Tyr Gln Glu Gly Thr Phe Arg Tyr Gly Ser Phe Lys Asp
 275 280 285
 Asp Gly Val Gln Val Leu Glu Leu Pro Tyr Lys Gly Asp Asp Ile Thr
 290 295 300
 Met Val Leu Val Leu Pro Ser Gln Glu Thr Pro Leu Thr Thr Val Glu
 305 310 315 320
 Gln Asn Leu Thr Leu Glu Lys Leu Gly Asn Trp Leu Gln Lys Ser Arg
 325 330 335
 Glu Leu Gln Leu Ser Val Tyr Leu Pro Arg Phe Arg Val Glu Asp Ser
 340 345 350
 Phe Ser Val Lys Glu Lys Leu Gln Glu Met Gly Leu Val Asp Ile Phe
 355 360 365
 Asp Pro Asn Ser Ala Lys Leu Pro Gly Ile Ile Ala Gly Gly Arg Thr
 370 375 380
 Asp Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn
 385 390 395 400
 Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Ile Leu Thr Gly
 405 410 415

ATTORNEY DOCKET NO. 21101.0021P1

Arg	Ser	Leu	Asn	Leu	Asn	Arg	Ile	Ile	Phe	Arg	Ala	Asn	Arg	Pro	Phe
							420		425						430
Leu	Val	Phe	Ile	Arg	Glu	Val	Ala	Ile	Asn	Ala	Ile	Leu	Phe	Met	Gly
							435		440						445
Arg	Val	Ala	Asn	Pro	Cys	Thr	Glu								
							450								455

<210> 90

<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 90

Met	Tyr	Ser	Pro	Gly	Ala	Gly	Ser	Gly	Ala	Ala	Gly	Glu	Arg	Lys	Leu
1				5				10							15
Cys	Leu	Leu	Ser	Leu	Leu	Leu	Ile	Gly	Ala	Leu	Gly	Cys	Ala	Ile	Cys
							20		25						30
His	Gly	Asn	Pro	Val	Asp	Asp	Ile	Cys	Ile	Ala	Lys	Pro	Arg	Asp	Ile
							35		40						45
Pro	Val	Asn	Pro	Leu	Cys	Ile	Tyr	Arg	Ser	Pro	Gly	Lys	Lys	Ala	Thr
							50		55						60
Glu	Glu	Asp	Gly	Ser	Glu	Gln	Lys	Val	Pro	Glu	Ala	Thr	Asn	Arg	Arg
65							70			75					80
Val	Trp	Glu	Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Asn	Phe	Tyr
							85		90						95
Gln	His	Leu	Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Ile	Phe	Leu	Ser	
							100		105						110
Pro	Leu	Ser	Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys
							115		120						125
Asn	Asp	Thr	Leu	Lys	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile
							130		135						140
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn
145							150			155					160
Cys	Arg	Leu	Tyr	Arg	Lys	Ala	Asn	Lys	Ser	Ser	Asp	Leu	Val	Ser	Ala
							165		170						175
Asn	Arg	Leu	Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Ser	Tyr	Gln
							180		185						190
Asp	Val	Ser	Glu	Val	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe
							195		200						205
Lys	Glu	Asn	Pro	Glu	Gln	Ser	Arg	Val	Thr	Ile	Asn	Asn	Trp	Val	Ala
							210		215						220
Asn	Lys	Thr	Glu	Gly	Arg	Ile	Lys	Asp	Val	Ile	Pro	Gln	Gly	Ala	Ile
225							230			235					240
Asn	Glu	Leu	Thr	Ala	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly
							245		250						255
Leu	Trp	Lys	Ser	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Pro	Phe	
							260		265						270
Tyr	Lys	Val	Asp	Gly	Gln	Ser	Cys	Pro	Val	Pro	Met	Met	Tyr	Gln	Glu
							275		280						285
Gly	Lys	Phe	Lys	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu
							290		295						300
Leu	Pro	Phe	Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys
305							310			315					320
Pro	Glu	Lys	Ser	Leu	Ala	Lys	Val	Glu	Gln	Glu	Leu	Thr	Pro	Glu	Leu
							325		330						335
Leu	Gln	Glu	Trp	Leu	Asp	Glu	Leu	Ser	Glu	Thr	Met	Leu	Val	Val	His
							340		345						350

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Met	Pro	Arg	Phe	Arg	Thr	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu
355						360						365			
Gln	Asp	Met	Gly	Leu	Ile	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Gln	Leu
370						375						380			
Pro	Gly	Ile	Val	Ala	Gly	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala
385						390					395				400
Phe	His	Lys	Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala
						405				410				415	
Ala	Ser	Thr	Ser	Val	Val	Ile	Thr	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg
						420				425				430	
Val	Thr	Phe	Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Leu	Ile	Arg	Glu	Val
						435				440				445	
Ala	Leu	Asn	Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val
						450				455				460	
Asn															
465															

<210> 91

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 91															
caccagcatc	atctcctcca	attcatccag	ctactctgcc	catgaagata	atagtttca										60
ggcggttgc	ctcagatcac	actatctcca	cttgcccagc	cctgtgaaag	attagcggcc										120
atgtatttcca	atgtgatagg	aactgttaacc	tctggaaaaaa	ggaagggtta	tcttttgtcc										180
ttgctgctca	ttggcttctg	ggactgcgtg	acctgtcacg	ggagccctgt	ggacatctgc										240
acagccaagg	cgcgggacat	tccccatgaat	cccatgtgca	tttaccgctc	cccgaggagaag										300
aaggcaactg	aggatgaggg	ctcagaacag	aagatcccg	aggccaccaa	ccggcgtgtc										360
tgggaactgt	ccaaggccaa	ttcccgcttt	gctaccactt	tctatcagca	cctggcagat										420
tccaaagaatg	acaatgataa	cattttcctg	tcacccctga	gtatctccac	ggcttttgc										480
atgaccaagg	tgggtgcctg	taatgacacc	cttcagcaac	tgtatggagg	atttaagtt										540
gacaccatat	ctgagaaaaac	atctgatcag	atccacttct	tctttcccaa	actgaactgc										600
cgactctatc	aaaaagccaa	caaattctcc	aagtttagtat	cagccaatcg	cctttttgga										660
gacaaatccc	ttaccccaa	tgagacctac	cagacatca	gtgagttgt	atatggagcc										720
aagctccagc	ccctggactt	caaggaaaat	gcagagcaat	ccagagcggc	catcaacaaa										780
tgggtgtcca	ataagaccga	aggccgaatc	accgatgtca	ttccctcgga	agccatcaat										840
gagctcaetg	ttctggtgct	ggttaacacc	atttactca	agggctgtg	gaagtcaaag										900
ttcagccctg	agaacacaag	gaaggaactg	ttctacaagg	ctgatggaga	gtcgttca										960
gcatctatga	tgtaccagga	aggcaaggtc	cgttatcgcc	gcgtggctga	aggcacccag										1020
gtgcttgagt	tgccttcaa	agggtatgac	atcaccatgg	tcctcatctt	gccccaaagct										1080
gagaagagcc	tggccaagggt	ggagaagaa	ctcaccccaag	aggtgtcgca	ggagtggctg										1140
gatgaatttg	aggagatgt	gctggtggtt	cacatcccc	gcttccgcat	tgaggacggc										1200
ttcagtttga	aggagcagct	gcaagacatg	ggccttgcg	atctgttcag	ccctgaaaag										1260
tccaaactcc	caggatttgt	tgcagaaaggc	cgagatgacc	tctatgtctc	agatgcattc										1320
cataaggcat	ttcttgaggt	aaatgaagaa	ggcagtgaag	cagctgcaag	taccgctt										1380
gtgattgtcg	gccgttcgt	aaaccccaac	agggtgactt	tcaaggccaa	caggcccttc										1440
ctggttttta	taagagaagt	tcctctgaac	actattatct	tcatgggcag	agtagccaa										1500
ccttgtgtta	agtaaaatgt	tcttatttctt	tgcacctt	ccttattttt	gtttgtgaac										1560
agaagtaaaa	ataaaatcaa	actacttcca	tctcacatt												1599

<210> 92

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

ATTORNEY DOCKET NO. 21101.0021P1

<223> Description of Artificial Sequence:/note =
synthetic construct

<221> VARIANT

<222> (386)...(389)

<223> Xaa = any amino acid

<400> 92

Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
1				5				10					15		
Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp	Glu
	20						25					30			
Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp	Glu
	35					40				45					
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His	Leu
	50					55			60						
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Ile	Phe	Leu	Ser	Pro	Leu	Ser	
	65				70			75					80		
Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp	Thr
		85				90				95					
Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu	Lys
		100				105				110					
Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu	
		115				120				125					
Tyr	Arg	Lys	Ala	Asn	Lys	Ala	Ser	Lys	Leu	Val	Ser	Ala	Asn	Arg	Leu
		130				135				140					
Phe	Gly	Asp	Lys	Ser	Leu	Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile	Ser	
	145				150			155					160		
Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys	Glu	Asn
		165				170				175					
Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn	Lys	Thr
		180				185					190				
Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Glu	Leu
		195				200				205					
Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu	Trp	Lys
		210				215				220					
Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys	Ala
	225				230				235				240		
Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly	Lys	Phe
		245				250				255					
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu	Pro	Phe
		260				265					270				
Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro	Glu	Lys
		275				280					285				
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln	Glu
		290				295				300					
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met	Pro	Arg
	305				310				315				320		
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln	Asp	Met
		325				330				335					
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro	Gly	Ile
		340				345					350				
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His	Lys
		355				360					365				
Ala	Phe	Leu	Glu	Val	Asn	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ser	Thr	
		370				375				380					
Ala	Xaa	Xaa	Xaa	Xaa	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr	Phe
	385				390					395				400	
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu	Asn
		405				410					415				

ATTORNEY DOCKET NO. 21101.0021P1

Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 93
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 93
Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
 1 5 10 15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
 20 25 30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
 35 40 45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
 50 55 60
Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser Pro Leu Ser
 65 70 75 80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
 85 90 95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
 100 105 110
Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
 115 120 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
 130 135 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
 145 150 155 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
 165 170 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
 180 185 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
 195 200 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
 210 215 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
 225 230 235 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
 245 250 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
 260 265 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
 275 280 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
 290 295 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
 305 310 315 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
 325 330 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
 340 345 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
 355 360 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
 370 375 380

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Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385 390 395 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
405 410 415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
420 425 430